

SEQUENCE LISTING

<110> Messier, Walter

<120> Methods to Identify Evolutionarily Significant Changes in Polynucleotide and Polypeptide Sequences in Domesticated Plants

<130> GENO200.1/CIP

<150> US 09/240,915

<151> 1999-01-29

<150> US 60/349,088

<151> 2002-01-16

<150> US 09/368,810

<151> 1999-08-03

<150> US 09/875,666

<151> 2001-06-06

<150> US 60/315,595

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<160> 91

<170> PatentIn version 3.1

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Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30
aaa gaa agg gaa aag gct gaa aag aag aaa gag aaa agg agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60
cac aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc 240
His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
65 70 75 80
cgg aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga 288
Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
85 90 95
ctc tca gaa gag cat gga gct cct tgc ttt act cag aca gag cat ggc 336
Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
100 105 110
tct cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta 384
Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
115 120 125
ccc agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata 432
Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile
130 135 140
aga aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt 480
Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val
145 150 155 160
gta caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt 528
Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser

2005/05/2000

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aaa caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val	210	215	220	672
cct cca tct atg agg gca tca aag gaa agg att ggc ctt cgt cct gca Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala	225	230	235	720
gag atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile	245	250	255	768
gtc aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct Val Asn Pro Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro	260	265	270	816
gcc aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His	275	280	285	864
ata gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys	290	295	300	912
ccg gaa gta cag ccc cca att ctg aag gtg cct gtg gct atg cct acc Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr	305	310	315	960
atc aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys	325	330	335	1008
tcc tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln	340	345	350	1056
tcc aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys	355	360	365	1104
aag ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met	370	375	380	1152
gat gat atg gat ctc ggg gac cag gat tgg ctg ctt gat agt acg agg Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg	385	390	395	1200

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Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His
420 425 430

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<212> PRT

<213> Oryza sativa cv. Azucena

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35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
65 70 75 80

Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
85 90 95

Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
100 105 110

Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
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Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile
130 135 140

Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val
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Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser
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Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr
180 185 190

Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro
195 200 205

Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val
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Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala
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Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile
245 250 255

Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro
260 265 270

Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His
275 280 285

Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys
290 295 300

Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr
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325 330 335

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340 345 350

Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys
355 360 365

Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met

370

375

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Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg
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Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu
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 <213> Oryza sativa cv. Nipponbare

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 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

aaa gaa agg gaa aag gct gaa aag aaa gag aaa agg agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
 35 40 45

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Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly			
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Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu			
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Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile			
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Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser			
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Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr			
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Ala Ser Thr Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro			
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Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val			
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Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala			
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Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile			
245	250	255	
gtc aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct			816
Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro			
260	265	270	
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Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His			

275

280

285

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 Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys
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912

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 Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr
 305 310 315 320

960

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 Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys
 325 330 335

1008

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1056

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1104

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1152

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1200

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 405 410 415

1248

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 420 425 430

1296

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1344

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Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
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His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
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Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
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Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
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Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
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Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile
130 135 140

Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val
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Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser
165 170 175

Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr
180 185 190

Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro
195 200 205

Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val
210 215 220

Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala
225 230 235 240

Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile
245 250 255

Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro
260 265 270

Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His
275 280 285

Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys
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Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr
305 310 315 320

Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys
325 330 335

Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln
340 345 350

Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys
355 360 365

Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met
370 375 380

Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg
385 390 395 400

Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu
405 410 415

Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His
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Leu Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 7

<211> 2461

<212> DNA

<213> Oryza sativa cv. Teqing

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卷之三

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aatcgtcagc agattgacac ctcgcagccc aaagaagagc cttgctcctc tggcaggaat 2100
gctgaagctg cttagtatac agtagagaag cagtccaaat cagatcgcaa aaagagccgc 2160
aaggctgaga agaaagagaa gaagttcaaa gatttatttg ttacctggga tcctccgtct 2220
atggaaatgg atgatatgga tcttgggac caggattggc tgcttggtag tacgaggaaa 2280
cctgatgctg gcattggcaa ctgcagagaa attgttgcact cacttacttc tcaatcagca 2340
gagcagttct cattgcagcc tagggcgatt catttaccag accttcatgt ctatcagttg 2400
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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gtg gtg gcc gtg gcc gcg gaa gca cag gca acc act aag ctc cag 96
Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu	85	90	95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser	100	105	110	336
cca gag agt tca cag gac agc aag aga aag aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	115	120	125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	130	135	140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	145	150	155	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	165	170	175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	180	185	190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	195	200	205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	210	215	220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	225	230	235	720
atg ttg gcc aat gtt ggt cct tca cca tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	245	250	255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	260	265	270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	275	280	285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro	290	295	300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc				960

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
 305 310 315 320

aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc 1008
 Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
 325 330 335

tct ggc agg aat gct gaa gct tca gta tca gta gag aag cag tcc 1056
 Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
 340 345 350

aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag 1104
 Lys Ser Asp Arg Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
 355 360 365

ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat 1152
 Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
 370 375 380

gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa 1200
 Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
 385 390 395 400

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act 1248
 Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
 405 410 415

tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta 1296
 Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
 420 425 430

cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1341
 Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
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 <213> Oryza sativa cv. Teqing

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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

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<213> Oryza sativa cv. Lemont

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gtgtgatccg ggggtgaggt taggccggac gccggggcat cagccatgtc gaggtgctc 180
ccctacccgc cgccggggta cgtcgaaac ccagtggtgg ccgtggccgc ggccgaagcg 240
caggcgacca ctaagggttg ttgaaccatc ggatttacac acgcacgtgc cggatcatt 300

gctcttcgcct	gttggtttg	atcgatctg	ttgggtgtgc	gtgtgtgatt	tggggatcgc	360
acgtgcgggg	aagctaacct	ttgcatggat	aacttgagat	ttgtgaggcc	gcgcttcgac	420
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<213>	Oryza sativa cv. Lemont

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ttcatcatta	ctatatattt	caaagaaaat	tctgcattgc	attcccgctcg	tccgttctaa	180
atcagaactg	acgattgctc	tggggctga	agctccagaa	agaaaggaa	aaggctgaaa	240
agaagaaaaga	gaaaaggagt	gacaggaaag	ctcttccaca	tggtgagata	tccaagcatt	300
caaagcgaac	ccaccacaag	aagagaaaac	atgaagacat	caataatgct	gatcagaagt	360
cccgaaaggt	ttcctccatg	gaacctggtg	agcaattgga	gaagagtgg	ctctcagaag	420
agcatggagc	tccttgctt	actcagacag	agcatggctc	tccagagagt	tcacaggaca	480
gcagcaagag	aagaaagggtt	gtgttaccca	gtcctagcca	agctaagaat	ggtgaggccc	540
tttcttgcat	ttgtcttctt	ttagctggtg	atgttgaatt	ggtttgactt	atcctgaatt	600
atcatcttgc	aggtaacatc	cttcgaataa	agataagaag	agatcaagat	tcttcagctt	660
ccctttcgga	gaaatcta	gttgtacaaa	caccagttca	tcaaattgg	tcaatgg	720
ctctgccaag	taagaaaaac	tcaatgcaac	cacacaacac	cgttatgt	gtgagaacag	780
catcaaccca	gcagcaaagc	atcaaagggt	atttcaagc	agtaccgaaa	caaggtatgc	840
caacccccagc	aaaagtcatg	ccaagagtcg	atgttccctcc	atctatgagg	gcatcaaagg	900
aaaggattgg	cttcgtcct	gcagagatgt	tggccaatgt	tggtcctca	ccctccaagg	960
caaaacagat	tgtcaatcct	gcagctgcta	agttacaca	aagagttgat	cctccacctg	1020
ccaaggccatc	tcaatggat	gtcctctgt	tgccatccaa	ggttcatata	gatgctactc	1080
gatctttac	gaaggcttcc	cagacagaga	tcaagccg	agtacagccc	ccaattctga	1140
aggtgcctgt	ggctatgcct	accatcaatc	gtcagcagat	tgacacctcg	cagccaaag	1200
aagagccttg	ctcctctggc	aggaatgctg	aagctgcttc	agtatcagta	gagaaggagt	1260
ccaagtcaga	tcgcaaaaag	agccgcaagg	ctgagaagaa	agagaagaag	ttcaaagatt	1320

tatggatctac ctgggatcct ccgttatgg aaatggatga tatggatctc ggggaccagg 1380
 attggctgct tgatagtacg aggaaacctg atgctggcat tggcaactgc agagaaattg 1440
 ttgatccact tacttctcaa tcagcagagc agttctcatt gcagcctagg gcgattcatt 1500
 taccagacct tcatgtctat cagttgccat atgtggttcc attcttagtt tgtgttagtga 1560
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gtg gtg gcc gtg gcc gcg gaa gcg cag gcg acc act aag ctc cag 96
 Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

aaa gaa agg gaa aag gct gaa aag aag aaa gag aaa agg agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Arg Ser Asp Arg
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

cac aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc 240
 His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser
 65 70 75 80

cgg aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga 288
 Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly
 85 90 95

ctc tca gaa gag cat gga gct cct tgc ttt act cag aca gag cat ggc 336
 Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly
 100 105 110

tct cca gag agt tca cag gac agc aag aga aga aag gtt gtg tta 384
 Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
 115 120 125

ccc agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata 432
 Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile

PAPILLOMAVIRUS

130

135

140

aga aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt			480
Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val			
145	150	155	160
gta caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt			528
Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser			
165	170	175	
aag aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca			576
Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr			
180	185	190	
gca tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ccg			624
Ala Ser Thr Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro			
195	200	205	
aaa caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt			672
Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val			
210	215	220	
cct cca tct atg agg gca tca aag gaa agg att ggc ctt cgt cct gca			720
Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala			
225	230	235	240
gag atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att			768
Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile			
245	250	255	
gtc aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct			816
Val Asn Pro Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro			
260	265	270	
gcc aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat			864
Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His			
275	280	285	
ata gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag			912
Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys			
290	295	300	
ccg gaa gta cag ccc cca att ctg aag gtg cct gtg gct atg cct acc			960
Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr			
305	310	315	320
atc aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc			1008
Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys			
325	330	335	
tcc tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag			1056
Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln			
340	345	350	
tcc aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag			1104
Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys			
355	360	365	

aag ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met 370 375 380	1152
gat gat atg gat ctc ggg gac cag gat tgg ctg ctt gat agt acg agg Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg 385 390 395 400	1200
aaa cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu 405 410 415	1248
act tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His 420 425 430	1296
tta cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Leu Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445	1344
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln 20 25 30	
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg 35 40 45	
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60	
His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser 65 70 75 80	
Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly 85 90 95	
Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly 100 105 110	

ACR72GK2000

Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu
115 120 125

Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile
130 135 140

Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val
145 150 155 160

Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser
165 170 175

Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr
180 185 190

Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro
195 200 205

Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val
210 215 220

Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala
225 230 235 240

Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile
245 250 255

Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro
260 265 270

Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His
275 280 285

Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys
290 295 300

Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr
305 310 315 320

Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys
325 330 335

Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln

340

345

350

Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys
355 360 365

Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met
370 375 380

Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg
385 390 395 400

Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu
 405 410 415

Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His
420 425 430

Leu Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

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<213> Oryza sativa strain IR64

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cgtgccggat catttgctct tgcctgttgg ttttgcgttgg atctgttggg tgtgcgttgt 180
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cccccaattc cgaagggtgcc tggctatg cctaccatca atcgtcagca gattgacacc 2040
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aagttcaaag atttatttgc tacctggat cctccgtcta tggaaatgga tgatatggat 2220
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tgcagagaaa ttgttgcatttcc acttacttct caatcagcgg agcagttctc attgcagcct 2340
agggcgattc atttaccaga cttcatgtc tatcagttgc catatgtgg tccattctag 2400
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 <212> DNA
 <213> Oryza sativa strain IR64

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gtg gtg gcc gtg gcc gcg gaa gca cag gca acc act aag ctc cag		96
Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln		
20 25 30		
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg		144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg		
35 40 45		
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac		192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His		
50 55 60		
aag aag aag aag cat gaa gac atc aat aat gct gat cag aag tcc cgg		240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg		
65 70 75 80		
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc		288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu		
85 90 95		
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct		336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser		
100 105 110		
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc		384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro		
115 120 125		
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga		432
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg		
130 135 140		
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta		480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val		
145 150 155 160		
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag		528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys		
165 170 175		

20% Tied

aaa aac tca atgcaa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act		1248	
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr			
405	410	415	
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta		1296	
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu			
420	425	430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag		1341	
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe			
435	440	445	
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<211> 446			
<212> PRT			
<213> Oryza sativa strain IR64			
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Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Arg Ser Asp Arg			
35	40	45	
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His			
50	55	60	
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg			
65	70	75	80
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu			
85	90	95	
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser			
100	105	110	
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro			
115	120	125	
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg			
130	135	140	
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val			

145

150

155

160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 17

<211> 2432

<212> DNA

<213> Oryza sativa cv. Kasalath

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<223> N = G or C

<220>

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<223> N = G or C

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acgtgccgga tcatttgctc ttgcctgtt gttttgatcg gatctgttgg ttgtgcgtgt 180

gtgatttggg gatcgcacgt gcgggaaagc taaccttgc atggataact tgagattgt 240

gaggccgcgc ttcgaccaga tcggtcgcca atcttttagt ggctgaccgt ggaaagagga 300

tattactgac cttcggtttt ctaattttgg ttgtgcgtt gaatctgaaa taaccagaat 360

agtcatgggg aaaaaagtct gatctggaag gttcgaatta catttctata tattgttgt 420

ctccccagacg atggttgcaa gaaattactc atgctggata aaattgtgga tgtaagagtc 480

tgcagttgtt aaaatctgga aacagcacat tttgccgtag taaatttcaa tccatgttgc 540

tgtctcgta ttggtgtgtt acgagtaacc tgtgttgtt tatctccgct tggactagat 600

tccaaagtaat ccagtgcctt catgacctgc aaattctatg cctatgaagt aacatgaaca 660

gttttatgt attctgttga tgcatacttg cattatttgt gagatgtaca tgttggtta	720
aaattttgca ttcaccatat agaaatagta actgactatc cttgtttagt tcgaaaacta	780
ctgcaggttt agttattctc tgttCCAAG agtgcttggtt atgattgtaa gggttacagt	840
tctgtgacta accatgtAAC aaatatatta aggattatca aattattcta tgtgaagtgt	900
ccgtGCCCTA attgtgttat cttctgtAAC tgatAGCACA acatttgttt cctgctgtgt	960
gcttGTGtaa attggtaCTT catcattACT atatATTCA aagAAAATTC tgcattGCAT	1020
tcccgtcgTC cgTTCTAAAT cagaACTgAC gattgctCTG gtggctGAAG ctccAGAAAG	1080
aaaggaaaaa ggCCGAAAAG aagaaAGAGA aaaggAGtGA cAGGAAAGCT cttccACATG	1140
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gtggactCTC agaAGAGCAT ggAGCTCCTT GCTTTACTCA GACAGTGCAT ggctctCCAG	1320
agAGTTCAcA ggACAGCAGC aAGAGAAGAA AGGTTGTTT ACCCAGTCCt AGCCAAGCTA	1380
agaatGGTGA ggCCCTTCTC tgcattGTC ttctttAGC tggTAGTGTt gaattGGTTT	1440
gacttatCCT gaattATCAT ctTGcAGGTA acatCCTCG AATAAGATA agaAGAGATC	1500
aagattCTC agCTTCCCTT tcggAGAAAT ctaatGTTGT ACAAAACACCA gttcatAAA	1560
tgggatCAGT ttCATCTCTG CCAAGTAAGA AAAACTCAAT GCAACCACAC AACACCGAAA	1620
tGATGGTGA aacAGCATCA ACCCAGCAGC AAAGCATCAA AGGTGATTT CAAGCAGTAC	1680
tGAAACAAGG tatGCCAACC CCAGAAAAG tcatGCCAAG AGTCGATGTT CCTCCATCTA	1740
tGAGGGCATC aaAGGAAAGG GTTGGCCTTC GTCCTGCAGA GATGTTGGCC AATGTTGGTC	1800
cttcaccCTC caaggAAAAA cAGATTGTCA atCCTGCAGC tgctaAGGTT acacAAAGAG	1860
ttgatCCTCC acCTGCCAAG GCACTCAGA GAATTGATCC TCTGTTGCCA tccaAGGTT	1920
atataGATGC tactCGATCT ttacGAAGN tctCCAGAC AGAGATCAAG CGGAAAGTAC	1980
AGCCCCAAT tccGAAGGTG CCTGTGGCTA tgcctaccat CAATCGTCAG CNGATTGACA	2040
cctcgcAGCC caaAGAAGAG CCTTGCTCTT CTGGCAGGAA TGCTGAAGCT GCTTCAGTAT	2100
cAGTAGAGAA GCACTGCCAAG tcaGATCGCA AAAAGAGCCG CAAGGCTGAG aAGAAAGAGA	2160
agaAGTTCAA agATTTATTt GTTACCTGGG atCCTCCGTC tatGAAATG GATGATATGG	2220
atCTTGGGGA ccaggATTGg CTGCTGGTA GTACGAGGAA ACCTGATGCT GGCATTGGCA	2280
actGCAGAGA aattGTTGAT CCACTTACTT CTCAATCAGC AGAGCAGTTC tcattGCAGC	2340

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aggtttgtgt agtgagatgg agtaggtgag aa 2432

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<212> DNA
<213> Oryza sativa cv. Kasalath

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<220>
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<222> (889)..(889)
<223> n = G, C

<220>
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<222> (971)..(971)
<223> n = A, T

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Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aaa gag aaa agg agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

cca gag agt tca cag gac agc aag aag aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	384
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	432
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	480
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	528
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	576
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	624
195 200 205	
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	672
210 215 220	
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	720
225 230 235 240	
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	768
245 250 255	
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	816
260 265 270	
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	864
275 280 285	
gat gct act cga tct ttt acg aag ntc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro	912
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	960
305 310 315 320	
aat cgt cag cng att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	1008
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<211> 446
<212> PRT
<213> Oryza sativa cv. Kasalath

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<223> The 'Xaa' at location 297 stands for Ile, Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (324)..(324)
<223> The 'Xaa' at location 324 stands for Gln, Arg, Pro, or Leu.

<220>
<221> misc_feature
<222> (889)..(889)
<223> n = G, C

<220>
<221> misc_feature
<222> (971)..(971)
<223> n = A, T

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Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

20% TGA
20% GAG
20% GAA
20% TGT

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

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<211> 2447
<212> DNA
<213> Oryza rufipogon strain 5948

UDC256.512.1

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 tttgttacct gggatcctcc gtctatggaa atggatgata tggatcttgg ggaccaggat 2220
 tggctgcttgc tagtacgag gaaacctgat gctggcatttgc gcaactgcag agaaattttt 2280
 gatccactta cttctcaatc agcggagcag ttctcatttgc agcctaggc gattcattta 2340
 ccagacccatc atgtctatca gttgcatat gtggccat tctaggtttgc tgtagtgaga 2400
 tggagtaggt gagaagttaga gagatgttgg gagagagctg tgtgggt 2447

<210> 21
 <211> 1341
 <212> DNA
 <213> Oryza rufipogon strain 5948

<220>
 <221> CDS
 <222> (1)..(1341)
 <223>

<220>
 <221> misc_feature
 <222> (1)..(15)
 <223> n = A, C, G, T

<400> 21
 nnn nnn nnn nnn ccc tac ccg ccg ccg ggg tac gtg cga aac cca 48
 Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15
 gtg gtg gcc gtg gcc gcg gaa gca cag gca acc act aag ctc cag 96
 Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30
 aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Arg Ser Asp Arg
 35 40 45

24/06/2001

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60	192
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80	240
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser 100 105 110	336
cca gag agt tca cag gac agc agc aag aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro 115 120 125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg 130 135 140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val 145 150 155 160	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys 165 170 175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816

2000-2001-2002-2003

aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415	1248
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430	1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445	1341

<210> 22
<211> 446
<212> PRT
<213> Oryza rufipogon strain 5948

<220>
<221> misc_feature
<222> (1)..(1)
<223> The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
yr, Trp, Cys, or Phe.

2000-2000-2000-2000

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<220>
<221> misc_feature
<222> (2)..(2)
<223> The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
      yr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (3)..(3)
<223> The 'Xaa' at location 3 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
      yr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (4)..(4)
<223> The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
      yr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (5)..(5)
<223> The 'Xaa' at location 5 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
      yr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (1)..(15)
<223> n = A, C, G, T

<400> 22
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Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Arg Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 23

<211> 146

<212> DNA

<213> Oryza rufipogon strain 5949

<400> 23

cccttacctc tgtgtgatcc gggggtgagc ttaggccgga cgccggggca tcagccatgt 60

cgaggtgctt cccctacccg ccgcgggggt acgtgcgaaa cccagtggtg gccgtggccg 120

cggccgaagc gcaggcgacc actaag 146

<210> 24

<211> 1615

<212> DNA

<213> Oryza rufipogon strain 5949

<400> 24

tctgtgacta accatgtaac aaatatatta aggattatca aattattcta tgtgaagtgt 60

ccgtgcctta attgtgttat cttctgtaac tgatagcaca acatttgttt cctgctgtgt 120

gcttgtgtaa attggactt catcattact atatattca aagaaaattc tgcattgcat 180

tcccgctgctc cgttctaaat cagaactgac gattgctctg gtggctgaag ctccagaaaag 240
 aaaggaaaaa ggccgaaaag aagaaagaga aaaagagtga cagggaaagct cttccacatg 300
 gtgagatatac caagcattca aagcgaaccc acaagaagag aaaacatgaa gacatcaata 360
 atgctgatca gaagtccccgg aaggtttcctt ccatggaaacc tggtgagcaa ttggagaaga 420
 gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac ggctctccag 480
 agagttcaca ggacagcagc aagagaagaa aggttgtt acccagtccct agccaagcta 540
 agaatggta gcccctttct tgcatttgc ttctcttagc tggtgatgtt gaattggttt 600
 gacttatcctt gaattatcat cttgcaggta acatccttcg aataaagata agaagagatc 660
 aagattcttc agcttccctt tcggagaaat ctaatgttgc acaaaccacca gttcatcaaa 720
 tgggatcagt ttcatctctg ccaagtaaga aaaactcaat gcaaccacac aacaccgaaa 780
 tcatggtag aacagcatca acccagcagc aaagcatcaa aggtgatgtt caagcagttac 840
 taaaacaagg tatgccaacc ccagcaaaag tcatgccaag agtgcgtt cctccatcta 900
 tgagggcatc aaaggaaagg gttggccttc gtcctgcaga gatgttgcc aatgttggtc 960
 cttcaccatc caaggcaaaa cagattgtca atcctgcagc tgctaaaggaa acacaaagag 1020
 ttgatcctcc acctgccaag gcatctcaga gaattgtatcc tctgttgcca tccaagggttc 1080
 atatagatgc tactcgatct ttacgaagg tctcccagac agagatcaag ccggaaagtac 1140
 agcccccaat tccgaaggtg cctgtggcta tgcctaccat caatcgtag cagattgaca 1200
 cctcgccagcc caaagaagag cttgctcctt ctggcaggaa tgctgaagct gcttcagtat 1260
 cagtagagaa gcagtccaaag tcagatcgca aaaagagccg caaggctgag aagaaagaga 1320
 agaagttcaa agatttattt gttacctggg atcctccgtc tatggaaatg gatgatatgg 1380
 atcttgggaa ccaggattgg ctgcttgta gtacgaggaa acctgatgtt ggcattggca 1440
 actgcagaga aattgttgat ccacttactt ctcaatcagc agagcagttc tcattgcagc 1500
 cttagggcgat tcatttacca gaccttcatg tctatcgtt gccatatgtg gttccattct 1560
 aggtttgtgt agtgagatgg agtaggtgag aagtagagag atgttgggag agagc 1615

<210> 25
 <211> 1341
 <212> DNA
 <213> Oryza rufipogon strain 5949

 <220>
 <221> CDS

<222> (1)..(1341)
<223>

<400> 25
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gtg gcc gtg gcc gcg gaa gca cag acc act aag ctc cag 96
Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

cca gag agt tca cag gac agc agc aag aga aag gtt gtg tta ccc 384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga 432
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta 480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag 528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca 576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa 624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca cca tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415	1248
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430	1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 26
<211> 446
<212> PRT
<213> Oryza rufipogon strain 5949

<400> 26

Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 27
<211> 107
<212> DNA
<213> Oryza rufipogon strain 5953

<400> 27
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acccagtggt ggccgtggcc gcggccgaag cgcaggcgac cactaag 107

<210> 28
<211> 1332
<212> DNA
<213> Oryza rufipogon strain 5953

<400> 28
ctccagaaag aaaggaaaaa ggccgaaaag aagaaagaga aaaagagtga cagggaaagct 60
cttccacatg gtgagatatac caagcattca aagcgaaccc acaagaagag aaaacatgaa 120
gacatcaata atgctgatca gaagtcccg aaggttcct ccatggaacc tggtagcaa 180
ttggagaaga gtggactctc agaagagcat ggagtcctt gcttactca gacagtgcac 240
ggctctccag agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtct 300
agccaagcta agaatggta ggccctttct tgcattttc ttcttttagc tggtagttt 360
gaattggttt gacttatcct gaattatcat cttgcaggtt acatccttcg aataaagata 420
agaagagatc aagattcttc agttccctt tcggagaaat ctaatgtgt acaaacacca 480
gttcatcaaa tggatcagt ttcatcttg ccaagtaaga aaaactcaat gcaaccacac 540
aacaccgaaa tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatttt 600
caagcagtac taaaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt 660
cctccatcta tgagggcatc aaaggaaagg gttggccttc gtcctgcaga gatgttggcc 720
aatgttggtc ctccaccctc caaggaaaaa cagattgtca atcctgcagc tgctaagggtt 780
acacaaagag ttgatcctcc acctgccaag gcatctcaga gaattgatcc tctgttgcca 840
tccaaggttc atatagatgc tactcgatct tttacgaagc tctccagac agagatcaag 900
ccggaagtac agccccaaat tccgaaggtg cctgtggcta tgcctaccat caatcgtag 960

cagattgaca cctcgccagcc caaagaagag ccttgctcct ctggcaggaa tgctgaagct 1020
 gcttcagtat cagtagagaa gcagtccaag tcagatcgca aaaagagccg caaggctgag 1080
 aagaaaagaga agaagttcaa agatttattt gttacctggg atcctccgtc tatggaaatg 1140
 gatgatatgg atcttggggg ccaggattgg ctgcttggta gtacgaggaa acctgatgct 1200
 ggcattggca actgcagaga aattgttcat ccacttactt ctcaatcage ggagcagttc 1260
 tcattgcagc ctagggcgat tcatttacca gaccttcatg tctatcagtt gccatatgtg 1320
 gttccattct ag 1332

<210> 29
 <211> 1341
 <212> DNA
 <213> Oryza rufipogon strain 5953

<220>
 <221> CDS
 <222> (1)..(1341)
 <223>

<400> 29
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

gtg gtg gcc gtg gcc gcg gaa gca cag gca acc act aag ctc cag 96
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
 20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
 50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
 Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
 65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288
 Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
 85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336
 Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
 100 105 110

cca gag agt tca cag gac agc agc aag aga aag gtt gtg tta ccc 384

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
 115 120 125
 agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga 432
 Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
 130 135 140
 aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta 480
 Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
 145 150 155 160
 caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag 528
 Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
 165 170 175
 aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca 576
 Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
 180 185 190
 tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa 624
 Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
 195 200 205
 caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct 672
 Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
 210 215 220
 cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag 720
 Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
 225 230 235 240
 atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc 768
 Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
 245 250 255
 aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc 816
 Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
 260 265 270
 aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata 864
 Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
 275 280 285
 gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg 912
 Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
 290 295 300
 gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc 960
 Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
 305 310 315 320
 aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc 1008
 Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
 325 330 335
 tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc 1056
 Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser

340 345 350

aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355	360	365	1104
tcc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380			1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400			1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415			1248
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430			1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1341
<210> 30 <211> 446 <212> PRT <213> Oryza rufipogon strain 5953			
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln 20 25 30			
Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg 35 40 45			
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60			
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80			
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95			

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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gtg gtg gcc gtg gcc gcg gaa gca cag gca acc act aag ctc cag 96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192

Lys	Ala	Leu	Pro	His	Gly	Glu	Ile	Ser	His	Ser	Lys	Arg	Thr	His		
50															60	
aag	aag	aga	aaa	cat	gaa	gac	atc	aat	aat	gct	gat	cag	aag	tcc	cgg	240
Lys	Lys	Arg	Lys	His	Glu	Asp	Ile	Asn	Asn	Ala	Asp	Gln	Lys	Ser	Arg	
65															80	
aag	gtt	tcc	tcc	atg	gaa	cct	ggt	gag	caa	ttg	gag	aag	agt	gga	ctc	288
Lys	Val	Ser	Ser	Met	Glu	Pro	Gly	Glu	Gln	Leu	Glu	Lys	Ser	Gly	Leu	
85															95	
tca	gaa	gag	cat	gga	gct	cct	tgc	ttt	act	cag	aca	gtg	cat	ggc	tct	336
Ser	Glu	Glu	His	Gly	Ala	Pro	Cys	Phe	Thr	Gln	Thr	Val	His	Gly	Ser	
100															110	
cca	gag	agt	tca	cag	gac	agc	agc	aag	aga	aga	aag	gtt	gtg	tta	ccc	384
Pro	Glu	Ser	Ser	Gln	Asp	Ser	Ser	Lys	Arg	Arg	Lys	Val	Val	Leu	Pro	
115															125	
agt	cct	agc	caa	gct	aag	aat	ggt	aac	atc	ctt	cga	ata	aag	ata	aga	432
Ser	Pro	Ser	Gln	Ala	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Ile	Lys	Ile	Arg	
130															140	
aga	gat	caa	gat	tct	tca	gct	tcc	ctt	tcg	gag	aaa	tct	aat	gtt	gta	480
Arg	Asp	Gln	Asp	Ser	Ser	Ala	Ser	Leu	Ser	Glu	Lys	Ser	Asn	Val	Val	
145															160	
caa	aca	cca	gtt	cat	caa	atg	gga	tca	gtt	tca	tct	ctg	cca	agt	aag	528
Gln	Thr	Pro	Val	His	Gln	Met	Gly	Ser	Val	Ser	Ser	Leu	Pro	Ser	Lys	
165															175	
aaa	aac	tca	atg	caa	cca	cac	aac	acc	gaa	atg	atg	gtg	aga	aca	gca	576
Lys	Asn	Ser	Met	Gln	Pro	His	Asn	Thr	Glu	Met	Met	Val	Arg	Thr	Ala	
180															190	
tca	acc	cag	cag	caa	agc	atc	aaa	ggt	gat	ttt	caa	gca	gta	ctg	aaa	624
Ser	Thr	Gln	Gln	Ser	Ile	Lys	Gly	Asp	Phe	Gln	Ala	Val	Leu	Lys		
195															205	
caa	ggt	atg	cca	acc	cca	gca	aaa	gtc	atg	cca	aga	gtc	gat	gtt	cct	672
Gln	Gly	Met	Pro	Thr	Pro	Ala	Lys	Val	Met	Pro	Arg	Val	Asp	Val	Pro	
210															220	
cca	tct	atg	agg	gca	tca	aag	gaa	agg	gtt	ggc	ctt	cgt	cct	gca	gag	720
Pro	Ser	Met	Arg	Ala	Ser	Lys	Glu	Arg	Val	Gly	Leu	Arg	Pro	Ala	Glu	
225															240	
atg	ttg	gcc	aat	gtt	ggt	cct	tca	cca	tcc	aag	gca	aaa	cag	att	gtc	768
Met	Leu	Ala	Asn	Val	Gly	Pro	Ser	Pro	Ser	Lys	Ala	Lys	Gln	Ile	Val	
245															255	
aat	cct	gca	gct	gct	aag	gtt	aca	caa	aga	gtt	gat	cct	cca	cct	gcc	816
Asn	Pro	Ala	Ala	Ala	Lys	Val	Thr	Gln	Arg	Val	Asp	Pro	Pro	Pro	Ala	
260															270	
aag	gca	tct	cag	aga	att	gat	cct	ctg	ttg	cca	tcc	aag	gtt	cat	ata	864
Lys	Ala	Ser	Gln	Arg	Ile	Asp	Pro	Leu	Leu	Pro	Ser	Lys	Val	His	Ile	

ORIGIN OF Oryza rufipogon

	275	280	285	
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro				912
290	295		300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile				960
305	310		315	320
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser				1008
325	330		335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Ala Ser Val Ser Val Glu Lys Gln Ser				1056
340	345		350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys Lys				1104
355	360		365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp				1152
370	375		380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys				1200
385	390		395	400
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr				1248
405	410		415	
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu				1296
420	425		430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe				1341
435	440		445	

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<213> Oryza rufipogon strain IRGCG105491

<400> 32

Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
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Val Val Ala Val Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
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Lys Glu Arg Glu Lys Ala Glu Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 33

<211> 180

<212> DNA

<213> Zea mays mays strain BS7

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ccgagccgga gtcgaccgct aaggttgtt gaaccttcgg atttacacac gcacgtgcac 120

gatcgtttgt tcaatctgta ggaaaaacccggatctgtgt gtttgcgcgt gcgtgatgtg 180
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 <213> Zea mays mays strain BS7
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 gaagaaaagag aaaaggagtg acaggaaagc tcccaagcag tgtgagacgt ccaaacattc 120
 aaagcacagc cataagaaga gaaagcttga agatgtcatc aaagctgagc agggtcccaa 180
 aagagtaccc aaagaatcag ttgagcagtt ggagaagagt ggactctcag aagagcatgg 240
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 gagacgaaag gttgtcctgt ccagtcctag ccaacctaag aatggtgaga ctattcttt 360
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 tattcatccc aacttgattt tacagggaaac attcttcgct tcaagattaa aagtagtcaa 480
 gayccccaat cagctgttct ggagaaacca agggttcttg agcaaccatt ggtccaacaa 540
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 attacagaat ccccgcaaa gaccatgcag agacttgtcc cccagcctgc agctaaggc 720
 acacatcctg ttgatcccc gtcagctgtt aaggtgccag ttggaaagatc gggcctacct 780
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 ccacctgtta agatgatgtc acagagagtt caccatccag cttccatggt gtcgcagaaa 900
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 gaagctaccc ggcctactgt tcttcaaaaa cccaggact tgcctgctat caagcagcag 1020
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 aaaaaagata agaagttcag agatctgttt gttacctgga atccggattt gatagagaat 1200
 gaaggttcag atcttggtga tgaagactgg ctgttcagca gtaaaaaggaa ctccgatgct 1260
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 aagccttctt tacaacccag ggcaacattt ttgccggacc ttaatatgtt ccagctgcca 1380
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agagctg 1447

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 <213> Zea mays mays strain BS7

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 gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

 cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

 cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gay 432
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

 ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160

 gtc caa caa atg gga tca ggt tca tcc cyg tcg ggc aag caa aat tca 528

Val Gln Gln Met Gly Ser Gly Ser Ser Xaa Ser Gly Lys Gln Asn Ser			
165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc			576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val			
180	185	190	
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg			624
Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro			
195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca			672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr			
210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg			720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser			
225	230	235	240
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga			768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg			
245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga			816
Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg			
260	265	270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt			864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe			
275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa			912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu			
290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc			960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile			
305	310	315	320
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc			1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe			
325	330	335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc			1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser			
340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag			1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys			
355	360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa			1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu			
370	375	380	
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac			1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn			

385	390	395	400	
tcc gat gtc atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro				1248
405	410	415		
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr				1296
420	425	430		
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe				1344
435	440	445		
taa				1347
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30				
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45				
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60				
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro 65 70 75 80				
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His 85 90 95				
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser 100 105 110				

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Xaa Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser

340

345

350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

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435 440 445

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<213> Zea mays mays strain HuoBai

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gccatcgta c gaaaagtccg aaaccaacta ttcaaattgg gattcattt ct tttttttt	780
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 2646

<210> 38
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 <213> Zea mays mays strain HuoBai

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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110
 cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125
 cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	480
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	528
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	576
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	624
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	672
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	720
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	768
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg	816
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	864
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	912
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	960
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe	1008
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	1056
340 345 350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	1104
355 360 365	

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	370 375 380	1152
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	385 390 395 400	1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	405 410 415	1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	420 425 430	1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe	435 440 445	1344
taa		1347
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Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45		
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60		
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro 65 70 75 80		
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His 85 90 95		
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser 100 105 110		

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 40
<211> 262
<212> DNA

<213> Zea mays mays strain Makki

<400> 40

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gagccggagt cgaccgctaa ggttttgtga accttcggat ttacacacgc acgtgccaga 180
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<213> Zea mays mays strain Makki

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atccgaattt gttgttgtat gatgggttggaa agtgactggc caaattttt tgttctcaa 180

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agttttcttt gacaaactgt ttgtcgagcg tcaattcgtt tttacctgaa ttactaatt	240
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln			
115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat			432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp			
130	135	140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg			480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu			
145	150	155	160
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca			528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser			
165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc			576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val			
180	185	190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg			624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro			
195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca			672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr			
210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg			720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser			
225	230	235	240
ggc cta cct ctg aag tct tcr gga agt gtg gac cct tcg cct gct aga			768
Gly Leu Pro Leu Lys Ser Xaa Gly Ser Val Asp Pro Ser Pro Ala Arg			
245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga			816
Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg			
260	265	270	
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Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe			
275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtc cta cca gaa			912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu			
290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc			960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile			
305	310	315	320
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc			1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe			
325	330	335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc			1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser			

340	345	350	
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355	360	365	
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370	375	380	
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385	390	395	400
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro			1248
405	410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr			1296
420	425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe			1344
435	440	445	
taa			1347
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<211> 448			
<212> PRT			
<213> Zea mays mays strain Makki			
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<222> (247)..(247)			
<223> The 'Xaa' at location 247 stands for Ser.			
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro			
1	5	10	15
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys			
20	25	30	
Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro			
35	40	45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg			
50	55	60	

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Xaa Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 44

<211> 125

<212> DNA

<213> Zea mays mays strain Min13

<400> 44

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cctacccgcc accggggtaac gtgcggaacc cagtggccgt ggccgagccg gagtcgaccg 120

ctaag 125

<210> 45

<211> 198

<212> DNA

<213> Zea mays mays strain Min13

<400> 45
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 tgtactgtat tgatgctgtt ttgtgtttct ttgttcggag cagcattcaa tgctcccttt 120
 gttgttttag agaatctgat atttgccatc gtaccgaaag tccgaaacca actattcaaa 180
 ttgggatttc atttcttt 198

<210> 46
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 <213> Zea mays mays strain Min13

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 cagttgagca gttggagaag agtggactct cagaagagca tggagctcct tctttgtac 600
 atacgataacg tgactctcct gagagctcac aggacagccg caagagacga aaggttgtcc 660
 tgtccagtcc tagccaaacct aagaatggtg agactattct cttgttttg ctattctgtat 720
 tgattttta ttatagaaga aatcaatcgc ttgttcagga ttttattcat cccaaacttga 780
 ttttacagga aacattcttc gcttcaagat taaaagtagt caagatcccc aatcagctgt 840
 tctggagaaa ccaagggttc ttgagcaacc attggtccaa caaatggat caggttcatc 900
 cctgtcgggc aagcaaattt caatccatca taagatgaat gtgagatcta cctctggta 960
 gcgagggttc aatggtgact cccaaagcgt aaaaaatgt ttgattacag aatccccggc 1020
 aaagaccatg cagagacttg tccccagcc tgcagctaa gtcacacatc ctgttgatcc 1080
 ccagtcagct gttaaggtgc cagttgaaag atcgggccta cctctgaagt cttcgggaag 1140
 tgtggaccct tcgcctgcta gagttatgag aagatttgat cctccacctg ttaagatgat 1200
 gtcacagaga gttcaccatc cagcttccat ggtgtcgtag aaagttgatc ctccgtttcc 1260

gaaggattata cataaggaaa ccggatctgt tgttcgcccta ccagaagcta cccggcctac 1320
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 cagagatctg tttgttacct ggaatccggt attgatagag aatgaaggtt cagatcttgg 1560
 tcatgaagac tggctgttca gcagtaaaag gaactccgat gctatcatgg ttcaaagcag 1620
 agctactgat agttcagtgc cgatccatcc aatggtgcag cagaagcctt ctttacaacc 1680
 cagggcaaca ttttgccgg accttaatat gtaccagctg ccatatgtcg taccattta 1740
 aacatctggc gaggtagatg agaatttagat gagatgttgg gagagag 1787

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 <212> DNA
 <213> Zea mays mays strain Min13

<220>
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336

100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe	1008

	325	330	335	
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	340	345	350	1056
cgg tca gay atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	355	360	365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	370	375	380	1152
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	385	390	395	1200
400				
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	405	410	415	1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	420	425	430	1296
435				
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe	440	445		1344
taa				1347
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<211> 448				
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro	1	5	10	15
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys	20	25	30	
Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro	35	40	45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg	50	55	60	
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro				

65

70

75

80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
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<213> Zea mays mays strain Pira

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ccttcggatt tacacacgca cgtgccagat ctttttcaa tctgttagtt ttgcgcggat 180
ctgtggtttgc cgcgtgcgtt atgtgggtat tgscctgttcc ttgaaagctt accgagctta 240
ggaagtgtat ggatcttgcgtt tagctgcacg aggtcccttcca aatcgattgt aaaatttaag 300
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atcggggaca ttgaaagaat ggtagaacat caaattcgat tcaaaaactgt gctagatttg 420

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ggtttggaaata tgagc	495
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cgcaatgcta cattcattct ttgtgttcgt gtaaatatca ttatacataa aaatgctgct	300
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gaaagaaaag gaaaaagccg aaaagaagaa agagaaaagg agtgcacagga aagctccaa	420
gcagtgtgag acgtccaaac attcaaagca cagccataag aagagaaagc ttgaagatgt	480
catcaaagct gagcagggtc cccaaagagt acccaaagaa tcagttgagc agttggagaa	540
gagtggactc tcagaagagc atggagctcc ttctttgtt catacgatac gtgactctcc	600
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ccgatccatc caatggtgca gcagaagcct tctttacaac ccagggcaac atttttgccg	1680
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<400> 51
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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag      96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
          20           25           30

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gaa aaa gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

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aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga      192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
   50           55           60

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aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc      240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65           70           75           80

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aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

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gg a gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca      336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
    100          105          110

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cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln			
115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat			432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp			
130	135	140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg			480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu			
145	150	155	160
gtc caa caa atg gga tca ggt tca tcc ctg tct ggc aag caa aat tca			528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser			
165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc			576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val			
180	185	190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg			624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro			
195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca			672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr			
210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg			720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser			
225	230	235	240
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga			768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg			
245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga			816
Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg			
260	265	270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt			864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe			
275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtc cta cca gaa			912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu			
290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc			960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile			
305	310	315	320
aag cag cag gag atc agg acc tct tyc tca aaa gaa gag ccc tgc ttc			1008
Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe			
325	330	335	
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Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser			

340	345	350	
cggtca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355			1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380			1152
gggtca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr 420 425 430			1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1344
taa			1347
<p><210> 52</p> <p><211> 448</p> <p><212> PRT</p> <p><213> Zea mays mays strain Pira</p>			
<p><220></p> <p><221> misc_feature</p> <p><222> (329)..(329)</p> <p><223> The 'Xaa' at location 329 stands for Ser, or Phe.</p>			
<400> 52			
Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro 1 5 10 15			
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30			
Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45			
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60			

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

<210> 53
<211> 212
<212> DNA
<213> Zea mays mays strain Sari

<400> 53
gcgcggcgtcgatccgtcgcatgtcgagggtgcttccccctacccgccaccggggtacgtgcgg 60

aaccccagtggccgtggccgagccggagtcgaccgctaaggtttgttgaaccttcggattt 120

acacacgcacgtgccagatcgtttgttcaaactctgttaggttttgcgccggatctgtggttt 180

cgcgctgcgtgatgtgggtattgcccggtcgat 212

<210> 54
<211> 1803
<212> DNA

<213> Zea mays mays strain Sari

<400> 54

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tggccctgta	tatcaatagc	aaccaacacc	atttatttag	cccatttttta	gttttcttgt	120
tctgttagagt	atgcattgtt	gcaggtctta	actgttgta	gggaagtaac	gtgttcaaca	180
tgattgtaaa	cgaataacaat	tctgttgcta	actgtgtaat	gatgagaagg	ataattgaat	240
aatctttgtg	aagtattact	gtctgaactg	tacgcaaatg	ctacattcat	tctttgtgtt	300
cgtgtaaata	tcattataca	taaaaatgct	gcattgcatt	cccgctgtcc	gttctaaatc	360
agaactgacg	attgctctgg	tggctgaagc	tcctgaaaga	aaaggaaaag	gccgaaaaga	420
agaaagagaa	aaggagtgac	aggaaagctc	ccaagcagtg	tgagacgtcc	aaacattcaa	480
agcacagcca	taagaagaga	aagcttgaag	atgtcatcaa	agctgagcag	ggtcccaaaa	540
gagtacccaa	agaatcagtt	gagcagttgg	agaagagtgg	actctcagaa	gagcatggag	600
ctccttcttt	tgtacatacg	atacgtgact	ctcctgagag	ctcacaggac	agcggcaaga	660
gacgaaaggt	tgtcctgtcc	agtccctagcc	aacctaagaa	tggtgagact	attctcttgt	720
ttttgttatt	ctgattgtt	tttttattata	gaagaaatca	atcgcttggtt	caggatttt	780
ttcatcccaa	cttgatttttta	cagggaaacat	tcttcgcttc	aagattaaaa	gtagtcaaga	840
tccccaaatca	gctgttctgg	agaaaccaag	ggttcttgag	caaccattgg	tccaacaaat	900
gggatcaggt	tcatccctgt	cgggcaagca	aaattcaatc	catcataaga	tgaatgtgag	960
atctacctct	ggtcagcgga	gggtcaatgg	tgactcccaa	gcagtacaaa	aatgtttgat	1020
tacagaatcc	ccggcaaaga	ccatgcagag	acttgtcccc	cagcctgcag	ctaaggtcac	1080
acatccgtt	gatccccagt	cagctgttaw	ggtgccagtt	ggaagatcg	gcctacctct	1140
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acctgttaag	atgatgtcac	agagagttca	ccatccagct	tccatggtgt	cgcagaaagt	1260
tgatccctcg	tttccgaagg	tattacataa	ggaaaccgg	tctgttgttc	gcctaccaga	1320
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aaaagataag	aagttcagag	atctgttgt	tacctgaaat	ccggatttga	tagagaatga	1560
agttcagat	cttggtgatg	aagactggct	gttcagcagt	aaaaggaact	ccgatgctat	1620

catggttcaa agcagagcta ctgatagttc agtgcgcgatc catccaatgg tgcagcagaa 1680
 gccttcttta caacccaggg caacattttt gccggacctt aatatgtacc agctgccata 1740
 tgtcgtagcca ttttaaacat ctggcgaggt agatgagaat tagatgagat gttgggagag 1800
 agc 1803

<210> 55
 <211> 1347
 <212> DNA
 <213> Zea mays mays strain Sari

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 55
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct qag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	480
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	528
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	576
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	624
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	672
210 215 220	
cat cct gtt gat ccc cag tca gct gtt awg gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser	720
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	768
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg	816
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	864
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	912
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	960
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe	1008
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg car gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	1056
340 345 350	
cgg tca gay atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	1104
355 360 365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380

ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
 Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
 Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445

taa 1347

<210> 56
 <211> 448
 <212> PRT
 <213> Zea mays mays strain Sari

<220>
 <221> misc_feature
 <222> (234)..(234)
 <223> The 'Xaa' at location 234 stands for Lys, or Met.

<400> 56

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 57
<211> 305
<212> DNA
<213> Zea mays mays strain Smena

<400> 57
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gtcggccatg tcgagggtct tccccatccc gccaccgggg tacgtgcgga acccagtggc 120
cgtggccgag ccggagtcga ccgctaaggt ttgttgaacc ttcggattta cacacgcacg 180
tgccagatcg tttgttcaat atgttaggttt tgccggatc tgtggttgc gcgtgcgtga 240
tgtgggtatt gcccgtgcct aagctaaccg agctgaggaa gtgtatggat cttgtgttagc 300
tgcac 305

<210> 58
<211> 2208
<212> DNA
<213> Zea mays mays strain Smena

<400> 58

2006-2010

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acagtatgtc gttatTTTgg gctaagcttg tgtaagaagg gtcgttgac attttgtact	240
gtattaatgc tgTTTGTgt ttcttgcgg gtagcagcat tcaatgctcc tttgttgg	300
tgagagaatc tgatatttgc catcgtaCCg aaagtccgaa accaactatt caaattggga	360
tttcatttct ttTTTTCT actgtttta gagttcttt tttcgctgct gtgctttgt	420
gggtcagtac gtgcatttct ctctttttt ctttttttt ctgatgttac tcttctgttgc	480
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tgtcagggaa gtaacgtgtt caacatgatt gtaaacgaat acaattctgt tgctaaactgt	660
gtaatgatga gaaggataat tgaatagtct ttgtgaagta ttactgtctg aactgtacgc	720
aatgctaca ttcatTTTGT gttcatgtaa atatcattat acataaaaat gctgcattgc	780
attcccgtcg tccgttctaa atcagaactg acgattgctc tggTggctga agctcctgaa	840
agaaaaggaa aaggccgaaa agaagaaga gaaaaggagt gacagggaaag atcccaagca	900
gtgtgagacg tccaaacact caaagcacag ccataagaag agaaagcttgc aagatgtcat	960
caaagctgag cagggTcccA aaagagtacc caaagaatca gttgagcagt tggagaagag	1020
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ttcaagattt aaagttagtca agatccccaa tcagctgttcc tggagaaacc aagggttctt	1320
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gttggaaagat cgggcctacc tctgaagtct tcaggaagtg tggacccttc gcctgctaga	1620
gttatgagaa gatttgatcc tccacctgtt aagatgtatgt cacagagagt tcaccatcca	1680
gcttccatgg tgcgcagaa agttgatcct ccgtttccgaa aggtattaca taaggaaacc	1740

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tctggtagga	atgcagaagc	tgttcaagtgc	caggatacta	agctctcccg	gtcagatatg		1920
aagaaaatcc	gcaaagctga	aaaaaaagat	aagaagttca	gagatctgtt	tgttacctgg		1980
aatccggtat	tgatagagaa	tgaaggttca	gatcttggtg	atgaagactg	gctgttcagc		2040
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atccatccaa	tggtgcagca	gaagccttct	ttacaaccca	ggcaacatt	tttgcggac		2160
cttaatatgt	accagctgcc	atatgtcgta	ccattttaaa	catctggc			2208

<210> 59
<211> 1640
<212> DNA
<213> Zea mays parviflumis strain Wilkes

<400> 59							
tcagggaaagt	aacgtgttca	acatgattgt	aaacgaatac	cattctgttgc	ctaactgtgt		60
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aatgctacat	tcattctttgc	tgttcgtgt	aatatcatta	tacataaaatg	ctgcattgca		180
ttcccgtcgt	ccgttctaaa	tcagaactga	cgattgctct	ggtggctgaa	gctcctgaaa		240
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caatcgcttgc	ttcaggattt	tattcatccc	aacttgattt	tacaggaaac	attttcgct		660
tcaagattaa	aagtgtcaa	gatccccat	cagctgttct	ggagaaacca	agggttcttgc		720
agcaaccatt	ggtccaacaa	atggatcag	gttcatccct	gtcgggcaag	aaaaattcaa		780
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cccagcctgc	agctaaggtc	acacatcctg	ttgatcccc	gtcagctgtt	aaggtgccag		960
ttggaagatc	gggcctacct	ctgaagtctt	cgggaaagtgt	ggacccttcg	cctgctagag		1020

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 gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa cccaaggact 1200
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 atccggattt gatagagaat gaaggttcag atcttggtga tgaagactgg ctgttcagca 1440
 gtaaaaggaa ctccgatgct atcatggttc aaagcagagc tactgatagt tcagtgccga 1500
 tccatccaat ggtgcagcag aagccttctt tacaacccag ggcaacattt ttgccggacc 1560
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<210> 60
 <211> 1347
 <212> DNA
 <213> Zea mays mays strain Smena

 <220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 60
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gat ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Asp Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

 gga gct cct tct ttt gta cat acg ata cgg gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

 cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
 115 120 125

 cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
 130 135 140

 ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
 145 150 155 160

 gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca 528
 Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
 165 170 175

 atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc 576
 Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
 180 185 190

 aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg 624
 Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
 195 200 205

 gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca 672
 Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
 210 215 220

 cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg 720
 His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
 225 230 235 240

 ggc cta cct ctg aag tct tca gga agt gtg gac cct tcg cct gct aga 768
 Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
 245 250 255

 gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga 816
 Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg
 260 265 270

 gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt 864
 Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
 275 280 285

 ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa 912
 Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

 gct acc ccg cct act gtt ctt caa aaa ccc aag gac ttg cct tct atc 960
 Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ser Ile

305	310	315	320	
aag cag cag gag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325		330	335	1008
tct ggt agg aat gca gaa gct gtt caa gtg cag gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340	345		350	1056
cg ^g tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355	360		365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370	375	380		1152
gg ^t tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385	390	395	400	1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405	410		415	1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr 420	425		430	1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe 435	440	445		1344
taa				1347
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<211> 448				
<212> PRT				
<213> Zea mays mays strain Smena				
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro 1 5 10 15				
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30				
Glu Lys Ala Glu Lys Lys Glu Lys Lys Arg Ser Asp Arg Lys Asp Pro 35 40 45				
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg				

50

55

60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ser Ile
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 62

<211> 893

<212> DNA

<213> Zea mays mays strain W22

<400> 62

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tcgtttgttc aatctgttagg ttttgcgcgg atctgtggtt tgcgcggtgc tgatgtggcc 180

ctgtgccttg aaagctaacc gagctgagga agtgttatgga tcttgtgttag ctgcacgagg 240

tcctccaaat cgattgtaaa atttaagttg tatggccggt aggccaagat tgggttagtc 300

cggtttcga aaactggtag catggttatc ggggacattg aaagaatggt agaacatcaa 360
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 aattcttaat acagtatttc gttatccc gctaagcttgc tgtaagaagg gtcgtttgac 600
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 ttttggttt tgagagaatc tgatattgc catcgatccg aaagtccgaa accaactatt 720
 caaatggga tttcatttct ttttctact gtttttagag ttctttttt cgctgctgtg 780
 ctcttgcgg tcagtacgtg catttcttctt ttttttctg atgttactct tctgttgacc 840
 aaaggagttc agaatttattt tggccctgta tatcaatagc aaccaacacc att 893

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 <211> 1411
 <212> DNA
 <213> Zea mays mays strain W22

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 gatgtcatca aagctgagca gggtccaaa agagtaccca aagaatcgt tgagcagttg 180
 gagaagagtg gactctcaga agagcatgga gtccttctt ttgtacatac gatacgtgac 240
 ttcctgaga gtcacagga cagcggcaag agacgaaagg ttgtcctgtc cagtcctagc 300
 caacctaaga atggtgagac tattcttttgc ttttgcatac tctgattgtat tttttattat 360
 agaagaaatc aatcgcttgc tcaggattttt attcatcccc acttgattttt acaggaaaca 420
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 aaaattcaat ccatcataag atgaatgtga gatctaccc tcgttgcgg aggggtcgatg 600
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 gacttgccttcc ccagcctgca gctaagggtca cacatcctgt tgatccccag tcagctgtta 720
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 ctgctagagt tatgagaaga tttgatcctc cacatgttac gatgtatgtca cagagatgtc 840
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agaaaaaccgg atctgttgtt cgcctaccag aagctacccg gcctactgtt cttcaaaaac 960
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 cctgcttctc tggtaggaat gcagaagcag ttcaagtgc a agatactaag ctctcccggt 1080
 cagacatgaa gaaaatccgc aaagctgaga aaaaagataa gaagttcaga gatctgttg 1140
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 tgttcagcag taaaaggaac tccgatgcta tcatggttca aagcagagct actgatagtt 1260
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 tgccggacct taatatgtac cagctgccat atgtcgtacc attttaaaca tctggcgagg 1380
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Zea mays mays strain W22

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 <213> Zea mays mays strain W22

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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag		96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys		
20 25 30		
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc		144
Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro		
35 40 45		
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga		192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg		
50 55 60		
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc		240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro		
65 70 75 80		
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat		288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His		
85 90 95		
gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca		336

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser			
100	105	110	
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa			384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln			
115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gac			432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp			
130	135	140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg			480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu			
145	150	155	160
gtc caa caa atg gga tca ggt tca tcc ccg tcg ggc aag caa aat tca			528
Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser			
165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag ccg agg gtc			576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val			
180	185	190	
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg			624
Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro			
195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca			672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr			
210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg			720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser			
225	230	235	240
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga			768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg			
245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga			816
Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg			
260	265	270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt			864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe			
275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa			912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu			
290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc			960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile			
305	310	315	320
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc			1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe			

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325	330	335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser			1056
340	345	350	

cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys		1104	
355	360	365	

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu		1152	
370	375	380	

ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn		1200	
385	390	395	400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro		1248	
405	410	415	

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr		1296	
420	425	430	

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe		1344	
435	440	445	

taa		1347
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<210> 65		
<211> 448		
<212> PRT		
<213> Zea mays mays strain W22		
<400> 65		

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro			
1	5	10	15

Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys			
20	25	30	

Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro			
35	40	45	

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg			
50	55	60	

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro		
---	--	--

65

70

75

80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 66
<211> 2644
<212> DNA
<213> Zea mays parviglumis strain Benz

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tcgtttgttc aatctgttagg ttttgcgcgg atctgtgggt tgccgcgtgcg tgatgtgggt 180
attgcccgtg ctttgaaagc taaccgagct gaggaagtgt atggatcttgc tgtagctgca 240
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atcaaattcg attcaaaaact gtgcttagatt tgcataattta gtcgccctaa aattacgtgg 420

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Zea mays parviflumis strain Benz

<210> 67
 <211> 1347
 <212> DNA
 <213> Zea mays parviflumis strain Benz

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<400> 67
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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

2015-05-24 10:00 AM

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser 100 105 110	336
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc	1008

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335
 tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc 1056
 Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350
 cggtca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104
 Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
 355 360 365
 ttca gaa gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152
 Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
 370 375 380
 gggtca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200
 Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
 385 390 395 400
 tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248
 Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
 405 410 415
 atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430
 tttttgccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
 435 440 445
 taa 1347

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 <211> 448
 <212> PRT
 <213> Zea mays parviglumis strain Benz

 <400> 68

 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290	295	300
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile		
305	310	315
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe		
325	330	335
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser		
340	345	350
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys		
355	360	365
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu		
370	375	380
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn		
385	390	395
400		
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro		
405	410	415
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr		
420	425	430
435		
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe		
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<213> Zea mays parviglumis strain BK4		
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cgtgccagat cgtttgttca atctgttagt ttgcgcgga tctgtggttt gcgcgtgcgt 180		
gatgtggccc gtgccttgaa agctaaccga gctgaggaag tgtatggatc ttgtgttagct 240		
gcacgaggc tccaaatacg attgtaaaat ttaagttgta tggccggtag gccaagattg 300		
ggtttagtccg gtttcgaaa actggtagca tggttatcg ggacattgaa agaatggtag 360		

aacatcaa at tcgattcaaa actgtgctag atttgcatat ttagtcgccc taaaattacg 420
 tggacgtggg tgatccgaat tggttgttgc atgatggttg gaagtgactg gccaaatttt 480
 ttgtttctca aagttttctt tgaaaaactg tttgtcgagc gtcaattcgt atttacctga 540
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 <211> 1775
 <212> DNA
 <213> Zea mays parviglumis strain BK4

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 accatttatt gatcccattt ttagtttct tggctgttag agtatgcatt gttgcaggtc 120
 ttaactgttg tcagggaaat aacgtgttca acatgattgt aaacaatac aattctgtt 180
 ctaactgtgt aatgatgaga aggataattt aataatctt gtgaagtatt actgtctgaa 240
 ctgtacgcaa atgctacatt cattttgtt gttcggtttaa atatcattat acataaaaat 300
 gctgcattgc attcccgatcg tccgttctaa tcagaactga cgattgtctt ggtggctgaa 360
 gctcctgaaa gaaaaggaaa aggccgaaaa gaagaaaagag aaaaggagtg acaggaaagc 420
 tcccaagcag tgtgagacgt ccaaaccattt aaagcacagc cataagaaga gaaagcttga 480
 agatgtcatc aaagctgagc agggtcccaa aagagtaccc aaagaatcag ttgagcagg 540
 ggagaagagt ggactcttag aagagcatgg agtccttctt tttgtacata cgatacgtga 600
 ctctccttag agctcacagg acagccgcaa gagacgaaag gttgtcctgt ccagtcctag 660
 ccaaccataag aatggtgaga ctattcttctt gttttgttta ttctgattga ttttttattta 720
 tagaagaaat caatcgcttgc ttcaggattt tattcatccc aacttgattt tacagggaaac 780
 attcttcgtt tcaagattaa aagtagtcaa gaccccaat cagctttctt ggagaaacca 840
 agggttcttgc agcaaccattt ggtccaaacaa atgggatcag gttcatcccc gtcgggcaag 900
 caaaatttcaa tccatcataa gatgaatgtg agatctaccc ctggtcagcg gagggtcgt 960
 ggtgactccc aagcagtaca aaaatgttttgc attacagaat ccccgccaa gaccatgcag 1020
 agacttgtcc cccagcctgc agctaaggc acacatcctt ttgatcccc gtcagctgtt 1080
 aagggtgccag ttggaaagatc gggcttaccc ctgaagtctt cggaaagtgtt ggacccttcg 1140
 cctgcttagag ttatgagaag atttgatcctt ccacctgttta agatgatgtc acagagagg 1200
 caccatccag ctccatggt gtcgcagaaa gttgatcctc cgtttccgaa ggtattacat 1260

aaggaaaccg gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa 1320
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 gttacctgga atccggatt gatagagaat gaaggttcag atcttggtga tgaagactgg 1560
 ctgttcagca gtaaaaggaa ctccgatgct atcatggttc aaagcagagc tactgatagt 1620
 tcagtgccga tccatccaat ggtgcagcag aagccttctt tacaacccag ggcaacattt 1680
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<210> 71
 <211> 1347
 <212> DNA
 <213> Zea mays parviflumis strain BK4

<220>
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 <222> (1)..(1347)
 <223>

<400> 71
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro
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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser

BIOCHEMIE

	100	105	110	
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	115	120	125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gac Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	130	135	140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	145	150	155	480
gtc caa caa atg gga tca ggt tca tcc ccg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Pro Ser Gly Lys Gln Asn Ser	165	170	175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	180	185	190	576
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	195	200	205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	210	215	220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	225	230	235	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	245	250	255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg	260	265	270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	275	280	285	864
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	290	295	300	912
gct acc cggt cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	305	310	315	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe	325	330	335	1008

Zea mays parviglumis strain BK4

tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350	1056
cggtca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380	1152
gggtca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400	1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415	1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr 420 425 430	1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445	1344
taa	1347
<210> 72	
<211> 448	
<212> PRT	
<213> Zea mays parviglumis strain BK4	
<400> 72	
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30	
Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60	
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro 65 70 75 80	

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
435 440 445

<210> 73
<211> 305
<212> DNA
<213> Zea mays parviglumis strain IA19

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cgtcggccat gtcgaggtgc ttcccctacc cgccaccggg gtacgtgcgg aaccaggtaggg 120
ccgtggccga gccggagtcg accgctaagg tttgttgaac cttcggattt acacacgcac 180
gtgccagatc gtttgttcaa tctgttagtt ttgcgcggat ctgtggtttg cgcgtgcgtg 240
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tagct 305

<210> 74

<211> 1309
<212> DNA
<213> Zea mays parviflumis strain IA19

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ggagctcctt ctttgtaca tacgatacgt gactctcctg agagctcaca ggacagcggc 180
aagagacgaa aggttgtcct gtccagtcct agccaaccta agaatggta gactattctc 240
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tttattcatc ccaacttgat tttacaggaa acattctcg cttcaagatt aaaagtagtc 360
aagatccccca atcagctgtt ctggagaaac caagggttct tgagcaacca ttggccaac 420
aaatggatc aggttcatcc ctgtcggca agcaaaattc aatccatcat aagatgaatg 480
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tgattacaga atccccggca aagaccatgc agagacttgt cccccagcct gcagctaagg 600
tcacacatcc tggatccc cagtcagctg ttaaggtgcc agttggaaga tcggcctac 660
ctctgaagtc ttcgggaagt gtggaccctt cgccctgtag agttatgaga agatggatc 720
ctccacctgt taagatgatg tcacagagag ttcaccatcc agcttccatg gtgtcgcaga 780
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cagttcaagt gcaggatact aagctctccc ggtcagacat gaagaaaatc cgcaaagctg 1020
agaaaaaaaaga taagaagttc agagatctgt ttgttacctg gaatccggta ttgatagaga 1080
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<210> 75
<211> 1347
<212> DNA
<213> Zea mays parviflumis strain IA19

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<222> (1)..(1332)
<223>

<220>

<221> misc_feature

<222> (82)..(168)

<223> n = A, C, T, or G

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1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag nnn nnn nnn nnn nnn 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa
20 25 30

nnn 144
Xaa
35 40 45

nnn nnn nnn nnn nnn nnn tca aag cac agc cat aag aag aga 192
Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag gtt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca 528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc 576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val

180	185	190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195	200	205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210	215	220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225	230	235	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245	250	255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg 260	265	270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275	280	285	864
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290	295	300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305	310	315	960
aag cag cag gak atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Xaa Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe 325	330	335	1008
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340	345	350	1056
cggtca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355	360	365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370	375	380	1152
gggtca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385	390	395	1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405	410	415	1248

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
 420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtcgtaccat tttaa 1347
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr
 435 440

<210> 76
<211> 444
<212> PRT
<213> Zea mays parviglumis strain IA19

<220>
<221> misc_feature
<222> (28)..(28)
<223> The 'Xaa' at location 28 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (29)..(29)
<223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (30)..(30)
<223> The 'Xaa' at location 30 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (31)..(31)
<223> The 'Xaa' at location 31 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (32)..(32)
<223> The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (33)..(33)
<223> The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (34)..(34)
<223> The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (35)..(35)
<223> The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (36)..(36)
<223> The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (37)..(37)
<223> The 'Xaa' at location 37 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (38)..(38)
<223> The 'Xaa' at location 38 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (39)..(39)
<223> The 'Xaa' at location 39 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (40)..(40)
<223> The 'Xaa' at location 40 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (41)..(41)
<223> The 'Xaa' at location 41 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>

<221> misc_feature
<222> (42)..(42)
<223> The 'Xaa' at location 42 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (43)..(43)
<223> The 'Xaa' at location 43 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (44)..(44)
<223> The 'Xaa' at location 44 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (45)..(45)
<223> The 'Xaa' at location 45 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (46)..(46)
<223> The 'Xaa' at location 46 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (47)..(47)
<223> The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (48)..(48)
<223> The 'Xaa' at location 48 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (49)..(49)
<223> The 'Xaa' at location 49 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature

<222> (50)..(50)
<223> The 'Xaa' at location 50 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (51)..(51)
<223> The 'Xaa' at location 51 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (52)..(52)
<223> The 'Xaa' at location 52 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (53)..(53)
<223> The 'Xaa' at location 53 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (54)..(54)
<223> The 'Xaa' at location 54 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (55)..(55)
<223> The 'Xaa' at location 55 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (56)..(56)
<223> The 'Xaa' at location 56 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (324)..(324)
<223> The 'Xaa' at location 324 stands for Glu, or Asp.

<220>
<221> misc_feature
<222> (82)..(168)
<223> n = A, C, T, or G

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

100%
00%
00%
00%

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Xaa Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr
435 440

<210> 77
 <211> 86
 <212> DNA
 <213> Zea mays parviglumis strain Wilkes

<400> 77
 ctctcgccgg gtagagcgc gtcgaccgt cggccatgtc gaggtgcttc ccctacccgc 60
 caccggggta cgtcgaaac ccagt 86

<210> 78
 <211> 1347
 <212> DNA
 <213> Zea mays parviglumis strain Wilkes

<220>
 <221> misc_feature
 <222> (52)..(81)
 <223> N = A, C, G, or T

<220>
 <221> CDS
 <222> (1)..(1347)
 <223>

<400> 78
 atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cg 48
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
 1 5 10 15

gtg nnn nnn nnn nnn nnn nnn nnn nnn nnn ctc ctg aaa gaa aag 96
 Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag a 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag qgt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc	1056

Ser	Gly	Arg	Asn	Ala	Glu	Ala	Val	Gln	Val	Gln	Asp	Thr	Lys	Leu	Ser	
340																350
cggtca	gacatg	aagaatc	cgcaaa	gctgag	aaa	aaagat	aag	aag								1104
Arg	Ser	Asp	Met	Lys	Lys	Ile	Arg	Lys	Ala	Glu	Lys	Lys	Asp	Lys	Lys	
355																365
tccaga	gatctgttt	acc	tgg	aatccg	gtatttg	ata	gag	aat	gaa							1152
Phe	Arg	Asp	Leu	Phe	Val	Thr	Trp	Asn	Pro	Val	Leu	Ile	Glu	Asn	Glu	
370																380
gggtca	gatcttgg	gatgaa	gac	tgg	ctgttc	agc	agt	aaa	agg	aac						1200
Gly	Ser	Asp	Leu	Gly	Asp	Glu	Asp	Trp	Leu	Phe	Ser	Ser	Lys	Arg	Asn	
385																400
tccgat	gctatc	atcgatg	gttcaa	agcaga	gctact	gat	agt	tca	gttgtc	ccg						1248
Ser	Asp	Ala	Ile	Met	Val	Gln	Ser	Arg	Ala	Thr	Asp	Ser	Ser	Val	Pro	
405																410
atccatcca	atgtgtgc	cagcag	aaggcc	ccttct	ttaaaa	cccagg	gcacaca									1296
Ile	His	Pro	Met	Val	Gln	Gln	Lys	Pro	Ser	Leu	Gln	Pro	Arg	Ala	Thr	
420																425
tttttttgc	ccgatctt	aatatgt	tac	cag	ctgttat	gtc	gtatccat									1344
Phe	Leu	Pro	Asp	Leu	Asn	Met	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Pro	Phe	
435																440
taa																1347
<210>	79															
<211>	448															
<212>	PRT															
<213>	Zea mays parviflumis strain Wilkes															
<220>																
<221>	misc_feature															
<222>	(18)..(18)															
<223>	The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.															
<220>																
<221>	misc_feature															
<222>	(19)..(19)															
<223>	The 'Xaa' at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.															
<220>																
<221>	misc_feature															
<222>	(20)..(20)															
<223>	The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.															
<220>																

<221> misc_feature
 <222> (21)..(21)
 <223> The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The 'Xaa' at location 22 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (23)..(23)
 <223> The 'Xaa' at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (24)..(24)
 <223> The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (25)..(25)
 <223> The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The 'Xaa' at location 26 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (27)..(27)
 <223> The 'Xaa' at location 27 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
 Tyr, Trp, Cys, or Phe.

 <220>
 <221> misc_feature
 <222> (52)..(81)
 <223> N = A, C, G, or T

 <400> 79

Met	Ser	Arg	Cys	Phe	Pro	Tyr	Pro	Pro	Gly	Tyr	Val	Arg	Asn	Pro
1				5			10					15		

Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys
20 25 30

Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
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ttacacacgc acgtgccaga tcgtttgttc aatctgttagg ttttgcgcgg atctgtggtt	180	
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caatcacttgc ttcaaggattt tattcatccc aacttgcattt tacaggaaac attcttcgt	720	
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 gtaaaaggaa ctccgatgct atcatggttc aaagcagagc tactgatagt tcagtgccga 1560
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aag 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcg caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga agg tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctc aag ttt tcg gga agt atg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Phe Ser Gly Ser Met Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg gga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Gly Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg tta Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag cag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Gln Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg cat gat act aag ctc tcc	1056

Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser			
340	345	350	
cgg tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag			1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys			
355	360	365	
tcc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa			1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu			
370	375	380	
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac			1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn			
385	390	395	400
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg			1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro			
405	410	415	
atc cat cca atk gtg cag cag aaa cct tct tta caa ccc agg gca aca			1296
Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr			
420	425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt			1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe			
435	440	445	
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Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro			
35	40	45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg			
50	55	60	

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Met Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Gln Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
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Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe
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<213> Zea luxurians

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cagatcgttt ggtcaatctg ttgggtttgc gcggatctgt ggtttgcgcg tgcgtgatgt 180
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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Pro Lys Glu Lys
 20 25 30
 gaa aag gcc gaa aag aag aaa gag aaa ccg agt gac agg aaa gct ccc 144
 Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
 35 40 45
 aag cag tgt gag acg tcc aaa cat tca aag cac atc cat aag aag aga 192
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg
 50 55 60
 aag ctt gaa gat gtc atc aaa gct ggg cag ggt ccc aaa aga gta ccc 240
 Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro
 65 70 75 80
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
 85 90 95
 gga gct cct tct ttt gta cat aag ata cgc gac tct cct gag agc tca 336
 Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser
 100 105 110
 cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln

2410032000T

115

120

125

432

cct aag aat gga aac att ctt cgc ttc aag att aaa agt aat caa gat
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Asn Gln Asp
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480

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gac caa cca ttg
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu
 145 150 155 160

528

gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca
 Val Gln Gln Met Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
 165 170 175

576

atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc
 Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
 180 185 190

624

aat ggt gaa tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg
 Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
 195 200 205

672

gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca
 Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
 210 215 220

720

cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg
 His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
 225 230 235 240

768

ggc cta cct ctg aag ttt tcg gga agt gtg gac cct tcg cct gct aga
 Gly Leu Pro Leu Lys Phe Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
 245 250 255

816

gtt atg gga aga ttt gat cct cca cct gtt aag atg atg tca cag aga
 Val Met Gly Arg Phe Asp Pro Pro Val Lys Met Met Ser Gln Arg
 260 265 270

864

gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg tta
 Val His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu
 275 280 285

912

ccg aag gta tta cat aag gaa acc gga tct gtt gtc cta cca gaa
 Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
 290 295 300

960

gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc
 Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
 305 310 315 320

1008

aag cag cag gag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc
 Lys Gln Gln Glu Ile Arg Thr Ser Ser Lys Glu Glu Pro Cys Phe
 325 330 335

1056

tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc
 Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
 340 345 350

cggtca gatgtg aagaaa atccgc aaa gct gagaaa aaaa gat aag aag Arg Ser Asp Val Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	355 360 365	1104
ttcaga gatctg tttgtt acc tgg aatccg gtgttg ataatagaa gat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	370 375 380	1152
ggtgtca gat ctt ggt gat gaa gac tgg ctgttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	385 390 395 400	1200
tcc gat gct atc atg gct caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	405 410 415	1248
atccat cca atg gtg cag cag aag cct tct ttg caa ccc agg gca acg Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	420 425 430	1296
ttt ttg ccg gac ctt aat atc tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Ile Tyr Gln Leu Pro Tyr Val Val Pro Phe	435 440 445	1344
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Glu Lys Ala Glu Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45		
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg 50 55 60		
Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro 65 70 75 80		
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His 85 90 95		

Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Asn Gln Asp
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val
180 185 190

Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser
225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Val Asp Pro Ser Pro Ala Arg
245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser
340 345 350

Arg Ser Asp Val Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn
385 390 395 400

Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr
420 425 430

Phe Leu Pro Asp Leu Asn Ile Tyr Gln Leu Pro Tyr Val Val Pro Phe
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<211> 21
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<213> Artificial Sequence primer

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<222> (1)..(21)
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<400> 87
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<213> Oryza sativa cv. Nipponbare

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